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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/024,686

DATE: 01/18/2002
TIME: 09:16:35

Input Set : N:\Crf3\RULE60\10024686.raw
Output Set: N:\CRF3\01182002\J024686.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Tsien, Roger Y.
6 Heim, Roger

8 (ii) TITLE OF INVENTION: MODIFIED GREEN FLUORESCENT PROTEINS

10 (iii) NUMBER OF SEQUENCES: 5

12 (iv) CORRESPONDENCE ADDRESS:

13 (A) ADDRESSEE: Fish & Richardson P.C.

14 (B) STREET: 4225 Executive Square, Suite 1400

15 (C) CITY: La Jolla

16 (D) STATE: CA

17 (E) COUNTRY: USA

18 (F) ZIP: 92037

20 (v) COMPUTER READABLE FORM:

21 (A) MEDIUM TYPE: Diskette

22 (B) COMPUTER: IBM Compatible

23 (C) OPERATING SYSTEM: Windiws95

24 (D) SOFTWARE: FastSEQ for Windows Version 2.0

26 (vi) CURRENT APPLICATION DATA:

C--> 27 (A) APPLICATION NUMBER: US/10/024,686

C--> 28 (B) FILING DATE: 17-Dec-2001

30 (vii) PRIOR APPLICATION DATA:

32 (A) APPLICATION NUMBER: 09/057,995

33 (B) FILING DATE:

35 (A) APPLICATION NUMBER: 08/727,452

36 (B) FILING DATE: 10-OCT-1996

38 (A) APPLICATION NUMBER: US95/14692

39 (B) FILING DATE: 13-NOV-1995

41 (A) APPLICATION NUMBER: 08/337,915

42 (B) FILING DATE: 10-NOV-1994

44 (viii) ATTORNEY/AGENT INFORMATION:

45 (A) NAME: Haile, Lisa A.

46 (B) REGISTRATION NUMBER: 38,347

47 (C) REFERENCE/DOCKET NUMBER: 07257/032002

49 (ix) TELECOMMUNICATION INFORMATION:

50 (A) TELEPHONE: 619/678-5070

51 (B) TELEFAX: 619/678-5099

54 (2) INFORMATION FOR SEQ ID NO: 1:

56 (i) SEQUENCE CHARACTERISTICS:

57 (A) LENGTH: 716 base pairs

58 (B) TYPE: nucleic acid

59 (C) STRANDEDNESS: double

60 (D) TOPOLOGY: linear

ENTERED

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62      (ii) MOLECULE TYPE: cDNA
64      (ix) FEATURE:
65          (A) NAME/KEY: Coding Sequence
66          (B) LOCATION: 1...715
69      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
71      ATG AGT AAA GGA GAA CTT TTC ACT GGA GTT GTC CCA ATT CTT GTT      48
72      Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
73      1          5          10          15
75      GAA TTA GAT GGT GAT GTT AAT GGG CAC AAA TTT TCT GTC AGT GGA GAG      96
76      Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
77      20          25          30
79      GGT GAA GGT GAT GCA ACA TAC GGA AAA CTT ACC CTT AAA TTT ATT TGC      144
80      Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
81      35          40          45
83      ACT ACT GGA AAA CTA CCT GTT CCA TGG CCA ACA CTT GTC ACT ACT TTC      192
84      Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
85      50          55          60
87      TCT TAT GGT GTT CAA TGC TTT TCA AGA TAC CCA GAT CAT ATG AAA CGG      240
88      Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg
89      65          70          75          80
91      CAT GAC TTT TTC AAG AGT GCC ATG CCC GAA GGT TAT GTA CAG GAA AGA      288
92      His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
93      85          90          95
95      ACT ATA TTT TTC AAA GAT GAC GGG AAC TAC AAG ACA CGT GCT GAA GTC      336
96      Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
97      100          105          110
99      AAG TTT GAA GGT GAT ACC CTT GTT AAT AGA ATC GAG TTA AAA GGT ATT      384
100     Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
101     115          120          125
103     GAT TTT AAA GAA GAT GGA AAC ATT CTT GGA CAC AAA TTG GAA TAC AAC      432
104     Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
105     130          135          140
107     TAT AAC TCA CAC AAT GTA TAC ATC ATG GCA GAC AAA CAA AAG AAT GGA      480
108     Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
109     145          150          155          160
111     ATC AAA GTT AAC TTC AAA ATT AGA CAC AAC ATT GAA GAT GGA AGC GTT      528
112     Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
113     165          170          175
115     CAA CTA GCA GAC CAT TAT CAA CAA AAT ACT CCA ATT GGC GAT GGC CCT      576
116     Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
117     180          185          190
119     GTC CTT TTA CCA GAC AAC CAT TAC CTG TCC ACA CAA TCT GCC CTT TCG      624
120     Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
121     195          200          205
123     AAA GAT CCC AAC GAA AAG AGA GAC CAC ATG GTC CTT CTT GAG TTT GTA      672
124     Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
125     210          215          220
127     ACA GCT GCT GGG ATT ACA CAT GGC ATG GAT GAA CTA TAC AAA TA      716
128     Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys

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129 225          230          235
132 (2) INFORMATION FOR SEQ ID NO: 2:
134   (i) SEQUENCE CHARACTERISTICS:
135       (A) LENGTH: 238 amino acids
136       (B) TYPE: amino acid
137       (D) TOPOLOGY: linear
139   (ii) MOLECULE TYPE: protein
141   (v) FRAGMENT TYPE: internal
143   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
145 Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
146   1          5          10          15
147 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
148       20          25          30
149 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
150       35          40          45
151 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
152       50          55          60
153 Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg
154       65          70          75          80
155 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
156       85          90          95
157 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
158       100         105         110
159 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
160       115         120         125
161 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
162       130         135         140
163 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
164       145         150         155         160
165 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
166       165         170         175
167 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
168       180         185         190
169 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
170       195         200         205
171 Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
172       210         215         220
173 Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
174 225          230          235
177 (2) INFORMATION FOR SEQ ID NO: 3:
179   (i) SEQUENCE CHARACTERISTICS:
180       (A) LENGTH: 22 base pairs
181       (B) TYPE: nucleic acid
182       (C) STRANDEDNESS: single
183       (D) TOPOLOGY: linear
185   (ii) MOLECULE TYPE: cDNA
187   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
189 GGATCCCCC GCTGAATTCA TG
192 (2) INFORMATION FOR SEQ ID NO: 4:

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22

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10024686.raw
Output Set: N:\CRF3\01182002\J024686.rawL:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]



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Team: OIPEBackFileIndexing
Dossier: 10024686

Legal Date: 06-04-2002

		Number of pages
No.	Dccode	
1	C.AD	2

Total number of pages: 2

Remarks:

Order of re-scan issued on